

Slobodzansky

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1652 RUSH

#5

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/952,741

DATE: 09/11/98
TIME: 15:49:27

Input Set: H952741.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Yuji, HATADA *new format*
2 Katsuya, OZAKI
3 Katsutoshi, ARA
4 Shuji, KAWAI
5 Susumu, ITO
6 <120> TITLE OF INVENTION: GENE ENCODING ALKALINE LIQUEFYING ALPHA-AMYLASE
7 <130> FILE REFERENCE: 2173-106P
8 <140> CURRENT APPLICATION NUMBER: US/08/952,741
9 <141> CURRENT FILING DATE: 1997-11-25
10 <160> NUMBER OF SEQ ID NOS: 11
11 <170> SOFTWARE: PatentIn Ver. 2.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 1776
14 <212> TYPE: DNA
15 <213> ORGANISM: Bacillus sp.
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (145)..(1692)
19 <400> SEQUENCE: 1
20 atataaattt gaaatgaaca cctatgaaaa tatggtagcg attgcgcac gagaaaaaac 60
21 ttgggagttt ggaagtgata ttaaaggatt tttttgact tggtgtaaa acgcttgcat 120
22 aaattgaagg agagggtgct tttt atg aaa ctt cat aac cgt ata att agc 171
Met Lys Leu His Asn Arg Ile Ile Ser
23 1 5
24 gta cta tta aca cta ttg tta gct gta gct gtt ttg ttt cca tat atg 219
25 Val Leu Leu Thr Leu Leu Ala Val Ala Val Leu Phe Pro Tyr Met
26 10 15 20 25
27 acg gaa cca gca caa gcc cat cat aat ggg acg aat ggg acc atg atg 267
28 Thr Glu Pro Ala Gln Ala His His Asn Gly Thr Asn Gly Thr Met Met
29 30 35 40
30 cag tat ttt gaa tgg cat ttg cca aat gac ggg aac cac tgg aac agg 315
31 Gln Tyr Phe Glu Trp His Leu Pro Asn Asp Gly Asn His Trp Asn Arg
32 45 50 55
33 tta cga gat gac gca gct aac tta aag agt aaa ggg att acc gct gtt 363
34 Leu Arg Asp Asp Ala Ala Asn Leu Lys Ser Lys Gly Ile Thr Ala Val
35 60 65 70
36 tgg att cct cct gca tgg aag ggg act tcg caa aat gat gtt ggg tat 411
37 Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr
38 75 80 85
39 ggt gcc tat gat ttg tac gat ctt ggt gag ttt aac caa aag gga acc 459
40 Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr
41 90 95 100 105
42 gtc cgt aca aaa tat ggc aca agg agt cag ttg caa ggt gcc gtg aca 507
43 Val Arg Thr Lys Tyr Gly Thr Arg Ser Gln Leu Gln Gly Ala Val Thr
44

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45	110	115	120	
46	tct ttg aaa aat aac ggg att caa gtt tat ggg gat gtc gtg atg aat			555
47	Ser Leu Lys Asn Asn Gly Ile Gln Val Tyr Gly Asp Val Val Met Asn			
48	125	130	135	
49	cat aaa ggt gga gca gac ggg aca gag atg gta aat gcg gtg gaa gtg			603
50	His Lys Gly Gly Ala Asp Gly Thr Glu Met Val Asn Ala Val Glu Val			
51	140	145	150	
52	aac cga agc aac cga aac caa gaa ata tca ggt gaa tac acc att gaa			651
53	Asn Arg Ser Asn Arg Asn Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu			
54	155	160	165	
55	gca tgg acg aaa ttt gat ttc cct gga aga gga aat acc cat tcc aac			699
56	Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr His Ser Asn			
57	170	175	180	185
58	ttt aaa tgg cgc tgg tat cat ttt gat ggg aca gat tgg gat cag tca			747
59	Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser			
60	190	195	200	
61	cgt cag ctt cag aac aaa ata tat aaa ttc aga ggt acc gca aag gca			795
62	Arg Gln Leu Gln Asn Lys Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala			
63	205	210	215	
64	tgg gac tgg gaa gta gat ata gag aac ggc aac tat gat tac ctt atg			843
65	Trp Asp Trp Glu Val Asp Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met			
66	220	225	230	
67	tat gca gac att gat atg gat cat cca gaa gta atc aat gaa ctt aga			891
68	Tyr Ala Asp Ile Asp Met Asp His Pro Glu Val Ile Asn Glu Leu Arg			
69	235	240	245	
70	aat tgg gga gtt tgg tat aca aat aca ctt aat cta gat gga ttt aga			939
71	Asn Trp Gly Val Trp Tyr Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg			
72	250	255	260	265
73	atc gat gct gtg aaa cat att aaa tac agc tat acg aga gat tgg cta			987
74	Ile Asp Ala Val Lys His Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu			
75	270	275	280	
76	aca cat gtg cgt aac acc aca ggt aaa cca atg ttt gca gtt gca gaa			1035
77	Thr His Val Arg Asn Thr Thr Gly Lys Pro Met Phe Ala Val Ala Glu			
78	285	290	295	
79	ttt tgg aaa aat gac ctt gct gca atc gaa aac tat tta aat aaa aca			1083
80	Phe Trp Lys Asn Asp Leu Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr			
81	300	305	310	
82	agt tgg aat cac tcc gtg ttc gat gtt cct ctt cat tat aat ttg tac			1131
83	Ser Trp Asn His Ser Val Phe Asp Val Pro Leu His Tyr Asn Leu Tyr			
84	315	320	325	
85	aat gca tct aat agt ggt ggc tat ttt gat atg aga aat att tta aat			1179
86	Asn Ala Ser Asn Ser Gly Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn			
87	330	335	340	345
88	ggt tct gtc gta caa aaa cac cct ata cat gca gtc aca ttt gtt gat			1227
89	Gly Ser Val Val Gln Lys His Pro Ile His Ala Val Thr Phe Val Asp			
90	350	355	360	
91	aac cat gac tct cag cca gga gaa gca ttg gaa tcc ttt gtt caa tcg			1275
92	Asn His Asp Ser Gln Pro Gly Glu Ala Leu Glu Ser Phe Val Gln Ser			
93	365	370	375	
94	tgg ttc aaa cca ctg gca tat gca ttg att ctg aca agg gag caa ggt			1323

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95 Trp Phe Lys Pro Leu Ala Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly
 96 380 385 390
 97 tac cct tcc gta ttt tac ggt gat tac tac ggt ata cca act cat ggt 1371
 98 Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly
 99 395 400 405
 100 gtt cct tcg atg aaa tct aaa att gat cca ctt ctg cag gca cgt caa 1419
 101 Val Pro Ser Met Lys Ser Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln
 102 410 415 420 425
 103 acg tat gcc tac gga acc caa cat gat tat ttt gat cat cat gat att 1467
 104 Thr Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His His Asp Ile
 105 430 435 440
 106 atc ggc tgg acg aga gaa ggg gac agc tcc cac cca aat tca gga ctt 1515
 107 Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser His Pro Asn Ser Gly Leu
 108 445 450 455
 109 gca act att atg tcc gat ggg cca ggg ggt aat aaa tgg atg tat gtc 1563
 110 Ala Thr Ile Met Ser Asp Gly Pro Gly Gly Asn Lys Trp Met Tyr Val
 111 460 465 470
 112 ggg aaa cat aaa gct ggc caa gta tgg aga gat atc acc gga aat agg 1611
 113 Gly Lys His Lys Ala Gly Gln Val Trp Arg Asp Ile Thr Gly Asn Arg
 114 475 480 485
 115 tct ggt acc gtc acc att aat gca gat ggt tgg ggg aat ttc act gta 1659
 116 Ser Gly Thr Val Thr Ile Asn Ala Asp Gly Trp Gly Asn Phe Thr Val
 117 490 495 500 505
 118 aac gga ggg gca gtt tcg gtt tgg gtg aag caa taaataagga acaagaggcg 1712
 119 Asn Gly Gly Ala Val Ser Val Trp Val Lys Gln
 120 510 515
 121 aaaattactt tcctacatgc agagcttcc gatcactcat acacccaata taaattggaa 1772
 122 gctt 1776
 123 <210> SEQ ID NO 2
 124 <211> LENGTH: 516
 125 <212> TYPE: PRT
 126 <213> ORGANISM: Bacillus sp.
 127 <400> SEQUENCE: 2
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 129 1 5 10 15
 130 Ala Val Ala Val Leu Phe Pro Tyr Met Thr Glu Pro Ala Gln Ala His
 131 20 25 30
 132 His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His Leu
 133 35 40 45
 134 Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala Asn
 135 50 55 60
 136 Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp Lys
 137 65 70 75 80
 138 Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp
 139 85 90 95
 140 Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
 141 100 105 110
 142 Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly Ile
 143 115 120 125
 144 Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Ala Asp Gly

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145	130	135	140
146	Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn Gln		
147	145	150	155
148	Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp Phe		160
149	165	170	175
150	Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr His		
151	180	185	190
152	Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys Ile		
153	195	200	205
154	Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Ile		
155	210	215	220
156	Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met Asp		
157	225	230	235
158	His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr Thr		240
159	245	250	255
160	Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His Ile		
161	260	265	270
162	Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr Thr		
163	275	280	285
164	Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu Ala		
165	290	295	300
166	Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val Phe		
167	305	310	315
168	Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly Gly		320
169	325	330	335
170	Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys His		
171	340	345	350
172	Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro Gly		
173	355	360	365
174	Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala Tyr		
175	370	375	380
176	Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr Gly		
177	385	390	395
178	Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser Lys		400
179	405	410	415
180	Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr Gln		
181	420	425	430
182	His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu Gly		
183	435	440	445
184	Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp Gly		
185	450	455	460
186	Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly Gln		
187	465	470	475
188	Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile Asn		480
189	485	490	495
190	Ala Asp Gly Trp Gly Asn Phe Thr Val Asn Gly Gly Ala Val Ser Val		
191	500	505	510
192	Trp Val Lys Gln		
193	515		
194	<210> SEQ ID NO 3		

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195 <211> LENGTH: 22
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: any n = a,c,t or g
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
202 <400> SEQUENCE: 3
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204 <210> SEQ ID NO 4
205 <211> LENGTH: 26
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: any n = a,c,t or g
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
212 <400> SEQUENCE: 4
W--> Of 213 tcrtgrtrt cnacraangt nacngc 26
214 <210> SEQ ID NO 5
215 <211> LENGTH: 23
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
220 <400> SEQUENCE: 5
221 agccaatctc tcgtatagct gta 23
222 <210> SEQ ID NO 6
223 <211> LENGTH: 22
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
228 <400> SEQUENCE: 6
229 gtacaaaaac accctataca tg 22
230 <210> SEQ ID NO 7
231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
236 <400> SEQUENCE: 7
237 aatggwacwa tgatgcakta 20
238 <210> SEQ ID NO 8
239 <211> LENGTH: 22
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
244 <400> SEQUENCE: 8

Input Set: H952741.RAW

Line	?	Error/Warning	Original Text
203	W	"N" or "Xaa" used: Feature required	tngaygcngt naarcayath aa
213	W	"N" or "Xaa" used: Feature required	tcrtgrttrt cnacraangt nacngc